



## **Diversity, structure, and novel physiologies in microbial communities in rapid sand filters**

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## DIVERSITY, STRUCTURE, AND NOVEL PHYSIOLOGIES IN MICROBIAL COMMUNITIES IN RAPID SAND FILTERS

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### DIVERSITY, STRUCTURE, AND NOVEL PHYSIOLOGIES IN MICROBIAL COMMUNITIES IN RAPID SAND FILTERS

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Rapid sand filtration (RSF) is frequently used to treat high-quality groundwater for drinking water production. Microbial density in RSFs is high and communities typically colonize the porous mineral matrix that coats the sand grains.

Microbes are assumed responsible for the removal of  $\text{NH}_4^+$ ,  $\text{Fe}^{2+}$ ,  $\text{Mn}^{2+}$ ,  $\text{CH}_4$ ,  $\text{H}_2\text{S}$  - the main constituents in groundwaters - although the details have remained obscure.

We have initiated a description of the diversity, abundance, and distribution of microbial communities across various RSFs, from which we have identified a core RSF microbiome, abundance of functional guilds, and spatial distribution patterns. Across all RSFs, *Nitrospira* abundance exceeded abundance of canonical Ammonium Oxidizing Bacteria (AOB).

Through metagenomic analysis, highly abundant composite population genomes belonging to the *Nitrospira* genus were recovered that harbor the metabolic capacity for complete ammonia oxidation (comammox).

DNA and RNA stable isotope probing (SIP) based on  $^{13}\text{C}$ -labeled bicarbonate incorporation was subsequently performed on RSF samples under continuous loading and with nitrification inhibitors.

SIP results provided the first insights into the *in situ* activity of comammox *Nitrospira* and novel nitrifiers in a complex microbiome.

Novel nitrifiers belonging to  $\alpha$  and  $\beta$  proteobacteria were detected as central players in nitrification in RSFs, supported by evidence from SIP and metagenomics.

Here, we are obtaining a first comprehensive insight into the phylogeny and physiology of the microbes that drive the nitrogen cycle in RSFs.